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RL J. BIOL. CHEM. 267:21172-21178(1992).
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNF-ALPHA AND
CC APPROXIMATELY 3-FOLD LOWER AFFINITY FOR TNF-BETA.
CC -1- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
CC LEVEL ON THREONINE RESIDUES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; M38215; G189186; -.
DR EMBL; M38587; G339752; -.
DR EMBL; M55944; G339758; -.
DR PIR; A35356; A35356.
DR PIR; A36007; A36007.
DR PIR; A36475; A36475.
DR PIR; B35010; B35010.
DR PIR; A23666; A23666.
DR HSSP; P19438; 1TNR.
DR MIM; 191191; -.
DR PROSITE; PS00652; TNFR-NGFR.
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL;
KW PHOSPHORYLATION.
FT SIGNAL 1 22
FT CHAIN 1 22
FT DOMAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT TRANSMEM 258 287 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 288 461 POTENTIAL.
FT DOMAIN 39 201 CYTOPLASMIC (POTENTIAL).
FT REPEAT 39 76 4 X TNFR-CYS.
FT REPEAT 77 118 TNFR-CYS 1.
FT REPEAT 119 162 TNFR-CYS 2.
FT REPEAT 163 201 TNFR-CYS 3.
FT DISULFID 40 53 TNFR-CYS 4.
FT DISULFID 54 67 BY SIMILARITY.
FT DISULFID 57 75 BY SIMILARITY.
FT DISULFID 78 93 BY SIMILARITY.
FT DISULFID 96 110 BY SIMILARITY.
FT DISULFID 100 118 BY SIMILARITY.
FT DISULFID 120 126 BY SIMILARITY.
FT DISULFID 134 143 BY SIMILARITY.
FT DISULFID 137 161 BY SIMILARITY.
FT DISULFID 164 179 BY SIMILARITY.
FT CARBOHYD 171 171 POTENTIAL.
FT CARBOHYD 193 193 POTENTIAL.
FT CONFLICT 141 141 R -> P (IN REF. 3).
FT CONFLICT 196 196 R -> T (IN REF. 1).
FT CONFLICT 363 363 A -> T (IN REF. 3).
SQ SEQUENCE 461 AA; 48316 MW; 0F5D0C44 CRC32;
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Query Match 13.4%; Score 405; DB 9; Length 461;
Best Local Similarity 41.8%; Pred. No. 1,33e-63;
Matches 69; Conservative 26; Mismatches 59; Indels 11; Gaps 8;
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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91187885.
RX LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,
RX WONG G.H., CHEN E.Y., GOEDEL D.V.;
RL PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91246168.
RA GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,
RA COPELAND N.G., JENKINS N.A., SMITH C.A.;
RL MOL. CELL. BIOL. 11:3020-3026(1991).
CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; M60469; G199828; -.
DR EMBL; M59378; G202095; -.
DR PIR; B38634; B38634.
DR HSSP; P19438; 1TNR.
DR PROSITE; PS00652; TNFR-NGFR.
KW RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL;
FT SIGNAL 1 22
FT CHAIN 1 22
FT DOMAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.
FT TRANSMEM 259 288 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 289 474 POTENTIAL.
FT DOMAIN 39 203 CYTOPLASMIC (POTENTIAL).
FT REPEAT 39 77 4 X TNFR-CYS.
FT REPEAT 78 119 TNFR-CYS 1.
FT REPEAT 120 164 TNFR-CYS 2.
FT REPEAT 165 203 TNFR-CYS 3.
FT DISULFID 40 54 TNFR-CYS 4.
FT DISULFID 57 75 BY SIMILARITY.
FT DISULFID 78 94 BY SIMILARITY.
FT DISULFID 96 110 BY SIMILARITY.
FT DISULFID 101 119 BY SIMILARITY.
FT DISULFID 121 127 BY SIMILARITY.
FT DISULFID 136 145 BY SIMILARITY.
FT DISULFID 139 163 BY SIMILARITY.
FT DISULFID 166 181 BY SIMILARITY.
FT CARBOHYD 69 69 POTENTIAL.
FT CARBOHYD 195 195 POTENTIAL.
SQ SEQUENCE 474 AA; 50319 MW; DC32B2B6 CRC32;
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Query Match 12.4%; Score 375; DB 9; Length 474;
Best Local Similarity 41.5%; Pred. No. 9.05e-57;
Matches 66; Conservative 21; Mismatches 61; Indels 11; Gaps 7;
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Db 45 yydqta-gmccskcspgqahkvcfctktsdtycdscsdtyltlmwvpcjlcsgcrssd 103
Oy 31 yDEETSHOLDKCPGTYLKQHCCTAKWTCVPCPDHYTDSMTSDCELYCSPVCKEL 90
Db 104 qvctacteqnrrictcrprgycaiskgqgcclcaplkrprfgfyatpqtstsvckpr 163
Oy 91 QVVKQECNTHNRVCEKGRY--LEI-EFC-L-RH-RSCPFGFVQAGTPEKNTVCKR 144
Db 164 cagpfntstsdicrphqicnvai--p-gnasrdvcsts 204
Oy 145 CPDGFESNETSSKAPCRKHTNCSVFGLLTQKGNATHDNCSGNS 189
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Db 52 gmcaakcprpgyvhfcmktsdtycadcaeamytqvwngftclscsscttdqvelrac 111
Oy 38 QLDCKCPGTYLKQHCCTAKWTCVPCPDHYTDSMTSDCELYCSPVCKELQVVKQEC 97
Db 112 tkqgnrvacacagyaalkthsgscrcgmrlskcprpfgyaassrapngvlykacagtf 171
Oy 98 NRTNHRVCEKGRY--LEIEF--CLKH-R-S-CPDGFVQAGTPEKNTVCKRCPDGF 150
Db 172 sdtstsdicrphicst--laip--gnastdvcaps 206
Oy 151 SNETSSKAPCRKHTNCSVFGLLTQKGNATHDNCSGNS 189
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OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89356608.
RA STAMENKOVIC I., CLARK E.A., SEED B.;
RL EMO J. 8:1403-1410(1989).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; X60592; G29851; -.
DR PIR; S04460; S04460.
DR MIM; 109535; -.
DR PROSITE; PS00652; TNFR_NGFR.
RW RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 277
FT DOMAIN 20 193 CD40L RECEPTOR.
FT TRANSMEM 194 215 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 216 277 POTENTIAL.
FT DOMAIN 25 187 CYTOPLASMIC (POTENTIAL).
FT REPEAT 25 60 4 X TNFR-CYS.
FT REPEAT 61 103 TNFR-CYS 1.
FT REPEAT 104 144 TNFR-CYS 2.
FT REPEAT 145 187 TNFR-CYS 3.
FT REPEAT 153 187 TNFR-CYS 4.
FT CARBOHYD 153 187 POTENTIAL.
FT CARBOHYD 180 180 POTENTIAL.
SQ SEQUENCE 277 AA; 30619 MW; 38284411 CRC32;

Query Match 10.0%; Score 303; DB 2; Length 277;
Best Local Similarity 36.8%; Pred. No. 1.03e-40;
Matches 56; Conservative 21; Mismatches 67; Indels 8; Gaps 7;

Db 38 cdicpgsgqlvscdefetecelcpcseselfdtmrethchqkycdpn-iglr-vqgkq 95
Oy 41 CDKCPGTYLKHCHTAKMTVCAPCPDHYYTDSWHTSDCC-L--YCSYCKELQYVKQEC 97
Db 96 tseidlticceagwhntseacescvlhscspgfygkqlatgvsdlcpcpvgffsnvs 155
Oy 98 NRTNHRVCECKEGRY-L-EI-EFLCKHRSCPGFGVAGTPERTVCKRCPDGFFSNET 154
Db 156 safekchpwtsctekdlvvgagagtnktvvcg 187
Oy 155 SSKAPCRKHTNCSVGLLTOKGNATHDNICS 186

TITLE 4
CD40_MOUSE STANDARD; PRT; 289 AA.
P27512;
DT 01-AUG-1992 (REL. 23, CREATED)
DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)
DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDM40).
GN CD40.
OS MUS MUSCULUS (MOUSE).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUHERIA; RODENTIA.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 92105763.
RA TORRES R.M., CLARK E.A.;
RL J. IMMUNOL. 148:620-626(1992).
RN [2]
RP REVISIONS.
RC STRAIN-BALB/C;
RA TORRES R.M.;
RL SUBMITTED (SEP-1996) TO EMBL/GENBANK/DBJ DATA BANKS.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=LIVER;
RX MEDLINE; 93094586.
RA GRIMALDI J.C., TORRES R., KOZAK C.A., CHANG R., CLARK E.A.,

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RA HOWARD M., COCKAYNE D.A.;
RL J. IMMUNOL. 149:3921-3926(1992).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; M83112; G1553059; -.
DR EMBL; M94126; G192526; -.
DR EMBL; M94128; G192526; JOINED.
DR EMBL; M94128; G192526; JOINED.
DR EMBL; M94127; G192526; JOINED.
DR PIR; A46476; A46476.
DR HSSP; P19438; 1TNR.
DR PROSITE; PS00652; TNFR_NGFR.
RW RECEPTOR; B-CELL; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.
FT SIGNAL 1 19
FT CHAIN 20 289
FT DOMAIN 20 193 CD40L RECEPTOR.
FT TRANSMEM 194 215 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 216 289 POTENTIAL.
FT DOMAIN 25 187 CYTOPLASMIC (POTENTIAL).
FT REPEAT 25 60 4 X TNFR-CYS.
FT REPEAT 61 103 TNFR-CYS 1.
FT REPEAT 104 144 TNFR-CYS 2.
FT REPEAT 145 187 TNFR-CYS 3.
FT REPEAT 153 187 TNFR-CYS 4.
FT CARBOHYD 153 187 POTENTIAL.
SQ SEQUENCE 289 AA; 32111 MW; D6D70A2C CRC32;

Query Match 9.7%; Score 294; DB 2; Length 289;
Best Local Similarity 38.8%; Pred. No. 9.50e-39;
Matches 59; Conservative 20; Mismatches 65; Indels 8; Gaps 6;

Db 38 cdicpgsrlshctalcitqchpcdsgefsaqwnrelrchnhcepn-qglr-vkheg 95
Oy 41 CDKCPGTYLKHCHTAKMTVCAPCPDHYYTDSWHTSDCC-LY--CSYCKELQYVKQEC 97
Db 96 taesdtctckegqgctskdeacaghtpccipgfygmamettctvchpccpvgffsnvs 155
Oy 98 NRTNHRVCECKEGRY-L-EI-EFLCKHRSCPGFGVAGTPERTVCKRCPDGFFSNET 154
Db 156 slfekcypwtscedknlvldkqtsqtnvicg 187
Oy 155 SSKAPCRKHTNCSVGLLTOKGNATHDNICS 186

RESULT 5
VT2_MXVYL STANDARD; PRT; 326 AA.
AC P29825;
DT 01-APR-1993 (REL. 25, CREATED)
DT 01-APR-1993 (REL. 25, LAST SEQUENCE UPDATE)
DT 01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN T2.
OS MYXOMA VIRUS (STRAIN LAUSANNE).
OC VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXYIRIDAE; CHORDOPOXYIRINAE;
OC LEPORIPOTVIRUSES.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91335768.
RA UPON C., MACEN J.L., SCHREIBER M., MCFADDEN G.;
RL VIROLOGY 184:370-382(1991).
CC -1- FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPEING THE POTENTIAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; M95181; G332310; -.
DR EMBL; A23729; E199442; -.
DR PIR; A40566; GOVZML.
DR HSSP; P19438; 1TNR.
DR PROSITE; PS00652; TNFR_NGFR.
RW RECEPTOR; GLYCOPROTEIN; REPEAT; SIGNAL.
FT SIGNAL 1 16
FT CHAIN 17 326 POTENTIAL.
FT DOMAIN 27 186 4 X TNFR-CYS.

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FT	REPEAT	27	62	TNFR-CYS 1.
FT	REPEAT	63	104	TNFR-CYS 2.
FT	REPEAT	105	147	TNFR-CYS 3.
FT	REPEAT	148	186	TNFR-CYS 4.
FT	CARBOHYD	66	66	POTENTIAL.
FT	CARBOHYD	181	181	POTENTIAL.
FT	CARBOHYD	205	205	POTENTIAL.
FT	CARBOHYD	238	238	POTENTIAL.
SO	SEQUENCE	326 AA:	35208 MW:	22059A61 CRC32:
Query Match				
Best Local Similarity 33.8%; Score 269; DB 10; Length 326;				
Matches 47; Conservative 25; Mismatches 58; Indels 9; Gaps 8;				
Db	40	ctscppgsaerlqgpgsdvtcspscknetfaastnbpacvscrgctqtnlsesgcdkt	99	
Qy	41	CDKPCPGYLYLQHCSTAKMKYCAACPDHYHYYDSHNTSDECLYCSPVCKELOYKQECNRT	100	
Db	100	rdrvcddsaagnyolkkgsgcgricapkckkagpagsvsghtlgtdivctkcpkrytsdav	158	
Qy	101	HNRCVCEKEGRT--LE-IEFC-L-KHRS-CPGPGGVVQAGIPERNYCKRCPPDGFSSNET	154	
Db	159	sstetclssfnysifevnl	177	
Qy	155	SSKAPCRKHTNC-SY-FGL	171	
RESULT	6	STANDARD:	PRF:	415 AA.
ID	TNRC_MOUSE			
AC	P50284;			
DT	01-OCT-1996 (REL. 34, CREATED)			
DT	01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)			
DT	01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)			
DE	LYMPHOTOXIN-BETA RECEPTOR PRECURSOR.			
GN	TNFR.			
OS	MUS MUSCULUS (MOUSE).			
OC	EUMETAZOA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; RODENTIA.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN-CYS; TISSUE-LUNG;			
RA	FORCE W.R., WILLIAMS-ABBOTT L., BRONNING J., HESSON C., TIZARD R.,			
RA	WARE C.F.;			
RL	SUBMITTED (JUN-1995) TO EMBL/GENBANK/DBJ DATA BANKS.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 96163885.			
RX	NAKAMURA T., TASHIRO K., NAZAREA M., NAKANO T., SASAYAMA S.,			
	HONDO T.;			
	GENOMICS 30:312-319(1995).			
CC	-1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN			
CC	IMMUNE DEVELOPMENT.			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
DR	EMBL; U29173; G681621; -			
DR	EMBL; L38423; G600223; -			
KW	RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.			
FT	CHAIN	1	30	POTENTIAL.
FT	DOMAIN	31	415	LYMPHOTOXIN-BETA RECEPTOR.
FT	TRANSSEM	224	244	POTENTIAL.
FT	DOMAIN	245	415	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	42	213	4 X TNFR-CYS.
FT	REPEAT	42	81	TNFR-CYS 1.
FT	REPEAT	82	124	TNFR-CYS 2.
FT	REPEAT	125	170	TNFR-CYS 3.
FT	REPEAT	171	213	TNFR-CYS 4.
FT	DISULFID	43	58	BY SIMILARITY.
FT	DISULFID	59	72	BY SIMILARITY.
FT	DISULFID	62	80	BY SIMILARITY.
FT	DISULFID	83	98	BY SIMILARITY.
FT	DISULFID	101	116	BY SIMILARITY.

FT	DISULFID	104	124	BY SIMILARITY.
FT	DISULFID	126	132	BY SIMILARITY.
FT	DISULFID	139	150	BY SIMILARITY.
FT	DISULFID	142	169	BY SIMILARITY.
FT	DISULFID	172	187	BY SIMILARITY.
FT	CARBOHYD	40	40	POTENTIAL.
FT	CARBOHYD	179	179	POTENTIAL.
SO	SEQUENCE	415 AA;	44956 MW; 3C5SD121 CRC32;	
Query Match				
Best Local Similarity		8.7%;	Score 265;	DB 9;
Matches		54;	Conservative	30;
			Mismatches	92;
			Indels	11;
			Gaps	8;
Db	52 epmhdcvccstrpmpgefifavcsrsqdcvtckctphnsnehmhlstcqlcrp.cdlvlgf	110		
QY	34 ETSQLLDCKCPPTGYLKHOTAKWKVCAPCPDHVYTDMSHNSDELYCSPOCKE-LQY	92		
Db	111 eevaprcsdtrkaercrcqpgmscvylndhevcchceerilvlpqptlaeavtdelndtynvc	170		
QY	93 VK-QECNRTHNRVCECKEGR---YLEIE--FCLKLR-S-CPREGV-VQAGTEPRNTYCK	143		
Db	171 pckpghfqtsparsprcqphtceiqglveaapqtsydcicknppegamlla1lsl	230		
QY	144 RCPGPFNSNERSNAKPRKHTNCVSFGLLLTKGNATHMDNIGCSNSSTQKCGIDVTLCE	203		
Db	231 vl1l1ft 237			
QY	204 EAFPRFA 210			
RESULT				
ID	V72_SFVKA	STANDARD;	PRT;	325 AA.
AC	P25943;			
DT	01-MAY-1992 (REL. 22, CREATED)			
DT	01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)			
DT	01-FEB-1994 (REL. 28, LAST ANNOTATION UPDATE)			
DT	TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).			
GN	T2.			
OS	SHOE FIBROMA VIRUS (STRAIN KAS2A) (SFV).			
OC	VIRIDAE; DS-DNA ENVELOPED VIRUSES; POXYIRIDAE; CHORDOPOXYIRINAE;			
OC	LEPORIPROVIRUSES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE; 87321103.			
RA	UPTON C., DELANGE A.M., MCFADDEN G.;			
RA	[2]			
RN	160:20-30(1987).			
RP	FUNCTION.			
RX	MEDLINE; 91207415.			
RA	SMITH C.A., DAVIS T., WIGNALL J.M., DIN W.S., FARRAH T., UPTON C.,			
RA	MCFADDEN G., GOODWIN R.G.;			
RL	BIOCHEM. BIOPHYS. RES. COMMUN. 176:335-342(1991).			
CC	-1- FUNCTION. BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO			
CC	RACH CELLULAR TARGET AND THEREBY DEAPENING THE POTENTIAL			
CC	ANTIVIRAL EFFECTS OF THE CYTOKINE.			
CC	-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
CC	EMBL; M17433; ; NOT ANNOTATED_CDS.			
DR	EMBL; A23727; E199408; --			
DR	PIR; B43692; B43692.			
DR	HSSP; P19438; 11NR.			
DR	PROSITE; PS00652; TNFR_NGFR.			
FW	RECEPTOR. GLYCOPROTEIN; REPEAT; SIGNAL.			
FT	SIGNAL	1	16	POTENTIAL.
FT	CHAIN	17	325	PROTEIN T2.
FT	DOMAIN	27	186	4 X TNFR-CYS.
FT	REPEAT	27	62	TNFR-CYS 1.
FT	REPEAT	63	104	TNFR-CYS 2.
FT	REPEAT	105	147	TNFR-CYS 3.
FT	REPEAT	148	186	TNFR-CYS 4.
FT	CARBOHYD	105	105	POTENTIAL.
FT	CARBOHYD	181	181	POTENTIAL.
FT	CARBOHYD	203	203	POTENTIAL.
FT	CARBOHYD	238	238	POTENTIAL.

Seq	SEQUENCE	3235 AA;	35132 MW;	G9D2C87B CRC32;
Query Match		8.6%;	Score 260;	DB 10;
Best Local Similarity		30.5%;	Pred. No. 1,976-31;	
Matches	51;	Conservative	31;	Mismatches 77; Indels 8; Gaps 5
Db	40	caschpgfyaaarlqgpgsntycspedgtffasthnapacvscrgpcghlseagpdcrt	99	
Qy	41	CDKCPGTYLKHCHTAKKRTVCAPCPDHYDTSWTSDECLTCSFVCKELOYVKECNR	100	
Db	100	hdvencstgnycllkagngcrlcapqtkcpagvvs-ghtragdtlcekphtysds1	158	
Qy	101	HNRVCECEGGR-L-EIE--FLCKHNSCPGFEVYVAGIPERTYVKRPDPGFFSNET	154	
Db	159	sptercgsfnyisvgnllypnetscett-aghneviktkeftv1	204	
Qy	155	SSKAPCRKHTNCSVFGILLTQGNATHDNICSGNSESPQKGGIDVTL	201	
UNT	8	STANDARD:	PRT:	435 AA.
AC	TNRC_HUMAN			P36941;
DT	01-JUN-1994	(REL. 29, CREATED)		
DT	01-JUN-1994	(REL. 29, LAST SEQUENCE UPDATE)		
DT	01-OCT-1996	(REL. 34, LAST ANNOTATION UPDATE)		
DE	LYMPHOTOXIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR			
DE	2 RELATED PROTEIN (TUMOR NECROSIS FACTOR C RECEPTOR).			
GN	TNFR.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=LAYER.			
RX	MEDLINE: 93252381.			
RA	BAENS M., CHAFERANET M., CASSIMAN J.J., DEN BERGHE H., MARIEN P.;			
RL	GENOMICS 16:214-218(1993).			
RN	[2]			
RP	FUNCTION.			
RX	MEDLINE: 94225209.			
RA	CROME P.D., VAN ARSDALE T.L., WALTER B.N., WARE C.F., HESSON C.,			
RA	EHEKNEBELS B., BROWNING J.L., DIN W.S., GOODWIN R.G., SMITH C.A.;			
RL	SCIENCE 264:707-710(1994).			
CC	-1- FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN			
CC	IMMUNE DEVELOPMENT.			
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.			
CC	-1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			
CC	EMBL; L04770; G339762; -.			
CC	MIM; 600979; -.			
CC	HSSP; P19999; ICUG.			
DR	PROSITE: PS00652; TNFR_NGFR.			
KW	RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.			
FT	SIGNAL	1	30	POTENTIAL.
FT	CHAIN	31	435	LYMPHOTOXIN-BETA RECEPTOR.
FT	DOMAIN	31	227	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	228	248	POTENTIAL.
FT	DOMAIN	249	435	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	42	211	4 X TNFR-CYS.
FT	REPEAT	42	81	TNFR-CYS 1.
FT	REPEAT	82	124	TNFR-CYS 2.
FT	REPEAT	125	168	TNFR-CYS 3.
FT	REPEAT	169	211	TNFR-CYS 4.
FT	DISULFD	43	58	BY SIMILARITY.
FT	DISULFD	59	72	BY SIMILARITY.
FT	DISULFD	62	80	BY SIMILARITY.
FT	DISULFD	83	98	BY SIMILARITY.
FT	DISULFD	101	116	BY SIMILARITY.
FT	DISULFD	104	124	BY SIMILARITY.
FT	DISULFD	126	132	BY SIMILARITY.
FT	DISULFD	139	148	BY SIMILARITY.
FT	DISULFD	142	167	BY SIMILARITY.
FT	DISULFD	170	185	BY SIMILARITY.
FT	CARBOHYD	40	40	POTENTIAL.

FT	CARBOHYD	177	177	POTENTIAL.
SO	SEQUENCE	435 AA;	46709 MW;	203B82DD CRC32:
	Query Match	8.6%;	Score 260;	DB 9; Length 435;
	Best Local Similarity	32.3%;	Pred. No. 1.97e-31;	
	Matches	52;	Conservative	23; Mismatches 75; Indels 11; Gaps 6
Db	52	epghricscrgpbtlyvsakscriidrtvcacatcaensynehwyltlcqlcrpcdgv-mgl	110	
QY	34	ETSHOLLCDKCPPGTYLKQHCTAKMKTKYACAPCPHYTDSMHTSDEC-LY--CSFVCKEL	90	
Db	111	eeiarp-ctskrtktqrcqgmifcaawalechcslldccpptyaealkdwygkninhcyp	169	
QY	91	QYVAOECPRTNRRVCECKEGRY-----LEIEFCLKHRSCEPGEFV-VQAGTPERNYCKR	144	
Db	170	ckaghfgntsspsarcphttrcengqilveaaprgadttc	210	
QY	145	CPDGFNETSSKAPCKRNTYCSVFGILLITQGNATHDNTC	185	
RESULT	9	STANDARD;	PRT;	349 AA.
ID	VC22_VARY	STANDARD;	PRT;	349 AA.
AC	P34015;			
DT	01-FEB-1994 (REL. 28, CREATED)			
DT	01-FEB-1994 (REL. 28, LAST SEQUENCE UPDATE)			
DT	01-JUN-1994 (REL. 29, LAST ANNOTATION UPDATE)			
DE	PROTEIN C22/B28 HOMOLOG.			
GN	GAR.			
OS	VARICOLA VIRUS.			
OC	VITIDAE; DS-DNA ENVELOPED VIRUSES; POXYVIRIDAE; CHORDOPOXYVIRINAE;			
OC	ORTHOPOXVIRUSES.			
RC	(1)			
RC	SEQUENCE FROM N.A.			
RC	STRAIN-INDIA-1967 / ISOLATE IND3:			
RX	MEDLINE; 93202281.			
RA	SHECHUKUNOV S.N., BLINOV V.M., SANDAKHCHIEV L.S.;			
RL	FEBS LETT. 319:80-83(1993).			
CC	1-1 SMILARITY: CONTAINS TWO LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGIONS.			
DR	EMBL; X69198; G457087; -			
DR	EMBL; X67117; G516449; -			
DR	PIR; D36858; D36858.			
DR	PIR; S35987; S35987.			
DR	PIR; S46888; S46888.			
DR	HSSP; P19438; TNFR.			
DR	PROSITE; PS00652; TNFR_NGFR.			
KR	REPEAT.			
FT	DOMAIN	31	108	2 X TNFR-CYS.
FT	REPEAT	31	66	TNFR-CYS 1.
FT	REPEAT	67	108	TNFR-CYS 2.
SO	SEQUENCE	349 AA;	38189 MW;	50DOB435 CRC32:
	Query Match	7.7%;	Score 233;	DB 10; Length 349;
	Best Local Similarity	32.0%;	Pred. No. 9.20e-26;	
	Matches	54;	Conservative	26; Mismatches 79; Indels 10; Gaps 7.
Db	1	mkvaylyilflscilngcraaaytpngkckdetykrhnlcslsppptyaarldsk	60	
QY	1	MNKLICALLVLD-ISIKWTQETFPFKYLYHDE-F-TSHOLLCDKCPPGTYLKQHCTAK	57	
Db	61	tnlgtcpsgqstfcsrnhlpaciscrgncsnqvetsctlnhricesspyyilk	120	
QY	58	MKTYCAPCPDHYHDSMHTSDECLCYCPVCKELDYVAOECPRTNRRVCECKEGRY--LE-	114	
Db	121	asgackacsgtkgilygvs-ghsvsdvvlscpsgdfityshvssadc	168	
QY	115	-IE--FCLKHRSCEPGEFVQAGTPERNYCKRCPDGFNETSSKAPC	160	
RESULT	10	STANDARD;	PRT;	454 AA.
ID	TNRL_MOUSE	STANDARD;	PRT;	454 AA.
AC	P25118;			
DT	01-MAY-1992 (REL. 22, CREATED)			
DT	01-MAY-1992 (REL. 22, LAST SEQUENCE UPDATE)			

DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).  
 GN TNFR1 OR TNFR-1.  
 OS MUS MUSCULUS (MOUSE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 91187885.  
 RA LEWIS M., TARTAGLIA L.A., LEE A., BENNETT G.L., RICE G.C.,  
 RA WONG G.H., CHEN E.Y., GOEDEL D.V.,  
 RA KONG G.H., CHEN E.Y., GOEDEL D.V.,  
 RA PROC. NATL. ACAD. SCI. U.S.A. 88:2830-2834(1991).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE: 91246168.  
 RA GOODWIN R.G., ANDERSON D., JERZY R., DAVIS T., BRANNAN C.I.,  
 RA COPELAND N.G., JENKINS N.A., SMITH C.A.,  
 RL MOL. CELL. BIOL. 11:3020-3026(1991).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE: 91285014.  
 RA BARRETT K., TAYLOR-FISHWICK D.A., COPE A.P., KISSONENGHIS A.M.,  
 RA GRAY P.W., FELDHAUS M., FOXWELL B.M.J.,  
 RA EUR. J. IMMUNOL. 21:1649-1656(1991).  
 RL [4]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE-SPLEEN;  
 RC MEDLINE: 92039815.  
 RA KOTHE J.G., BROCKHAUS M., GENTZ R., LESSLAUER W.,  
 RL IMMUNOGENETICS 34:338-340(1991).  
 RN [5]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE: 94245292.  
 RA BEBO B.F., LINTHICUM D.S.,  
 RL IMMUNOGENETICS 39:450-451(1994).  
 RN [6]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE: 93156721.  
 RA KOTHE J., BLUETMANN H., GENTZ R., LESSLAUER W., STEINMETZ M.,  
 RL MOL. IMMUNOL. 30:165-175(1993).  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL: M60468; G199826; -.  
 DR EMBL: M59377; G202097; -.  
 DR EMBL: X59238; G53579; -.  
 DR EMBL: X57796; G54849; -.  
 DR EMBL: L26349; G430733; -.  
 DR EMBL: M76656; G202102; -.  
 DR EMBL: M88067; G202102; JOINED.  
 DR EMBL: M76655; G202102; JOINED.  
 DR PIR: A36834; GDMST1.  
 DR PIR: S16677; S16677.  
 DR PIR: S19021; S19021.  
 DR HSSP: P19438; 1TNR.  
 DR PROSITE: PS00652; TNFR\_NGFR.  
 DR PROSITE: PS50017; DEATH\_DOMAIN.  
 DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.  
 KM RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.  
 FT SIGNAL 1 21  
 FT CHAIN 22 454  
 FT DOMAIN 22 212  
 FT TRANSSEM 213 235  
 FT DOMAIN 236 454  
 FT DOMAIN 43 196  
 FT REPEAT 43 82  
 FT REPEAT 83 125  
 FT REPEAT 126 166  
 FT REPEAT 167 196  
 FT REPEAT 167 196  
 FT DOMAIN 356 441  
 FT DISULFID 44 38  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99

FT DISULFID 102 117 BY SIMILARITY.  
 FT DISULFID 105 125 BY SIMILARITY.  
 FT DISULFID 127 143 BY SIMILARITY.  
 FT DISULFID 146 158 BY SIMILARITY.  
 FT DISULFID 149 166 BY SIMILARITY.  
 FT DISULFID 168 179 BY SIMILARITY.  
 FT DISULFID 182 191 BY SIMILARITY.  
 FT DISULFID 185 195 BY SIMILARITY.  
 FT CARBOHYD 54 54 POTENTIAL.  
 FT CARBOHYD 151 151 POTENTIAL.  
 FT CARBOHYD 202 202 POTENTIAL.  
 FT CONFLICT 394 394 R -> G (IN REF. 6).  
 SQ SEQUENCE 454 AA; 50129 MW; 4B6BEC09 CRC32;  
 Query Match 7.3%; Score 221; DB 9; Length 454;  
 Best Local Similarity 33.1%; Pred. No. 2,72e-23;  
 Matches 48; Conservative 21; Mismatches 65; Indels 11; Gaps 9;  
 Db 49 yvhsknslcctkqhkytvsdcsprdtcrecekgftlsgnylrgclscckrke 108  
 QY 31 YDETSQHLCDKCPPTVYKQHCITAK-WKTVCAPCPDHYTDSWHTSDCLTCSPVCKE 89  
 Db 109 msqvelspcqdxdvycgckengfrylsethfcydcspcng-tvtpcketnttvcn 167  
 QY 90 LQYVK-OECNRTNHRVCECKEG--RYL-EIEF-CLKHRCPPGFGVYQAGTPERNTVCK 143  
 Db 168 -chagfflirecevpchckkneec 191  
 QY 144 RCPDGFPSNETSSKA-P-CRKHNC 166  
 RESULT 11  
 ID TNFR1\_RAT STANDARD; PRT; 461 AA.  
 AC P22934;  
 DT 01-AUG-1991 (REL. 19, CREATED)  
 DT 01-MAR-1992 (REL. 21, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE TUMOR NECROSIS FACTOR RECEPTOR 1 PRECURSOR (P60) (TNF-R1) (P55).  
 GN TNFR1 OR TNFR-1.  
 OS RATRATTUS NORVEGICUS (RAT).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; RODENTIA.  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RP MEDLINE: 91090841.  
 RA HIMMELER A., MAURER-FOGY I., KROENKE M., SCHEURICH P., PFITZENMAIER K.,  
 RA LANTZ M., OLSSON I., HAUFMANN R., STRATOWA C., ADOLF G.R.,  
 RL DNA CELL. BIOL. 9:705-715(1990).  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL: M63122; G207362; -.  
 DR PIR: B36555; B36555.  
 DR HSSP: P19438; 1TNR.  
 DR PROSITE: PS00652; TNFR\_NGFR.  
 DR PROSITE: PS50017; DEATH\_DOMAIN.  
 DR RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.  
 KM RECEPTOR; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT; SIGNAL.  
 FT SIGNAL 1 21  
 FT CHAIN 22 455  
 FT DOMAIN 22 211  
 FT TRANSSEM 212 234  
 FT DOMAIN 235 461  
 FT DOMAIN 43 196  
 FT REPEAT 43 82  
 FT REPEAT 83 125  
 FT REPEAT 126 166  
 FT REPEAT 167 196  
 FT REPEAT 167 196  
 FT DOMAIN 363 448  
 FT DISULFID 44 58  
 FT DISULFID 59 72  
 FT DISULFID 62 81  
 FT DISULFID 84 99  
 FT DISULFID 102 117 BY SIMILARITY.

FT DISULFID 105 125 BY SIMILARITY.  
 FT DISULFID 127 143 BY SIMILARITY.  
 FT DISULFID 146 158 BY SIMILARITY.  
 FT DISULFID 149 166 BY SIMILARITY.  
 FT DISULFID 168 179 BY SIMILARITY.  
 FT DISULFID 182 191 BY SIMILARITY.  
 FT DISULFID 185 195 BY SIMILARITY.  
 FT CARBOHYD 54 54 POTENTIAL.  
 FT CARBOHYD 151 151 POTENTIAL.  
 FT CARBOHYD 201 201 POTENTIAL.  
 SQ SEQUENCE 461 AA; 50969 MW; 82F68B08 CRC32;

Query Match 7.3%; Score 220; DB 9; Length 461;  
 Best Local Similarity 33.8%; Pred. No. 4.35e-23;  
 Matches 49; Conservative 22; Mismatches 63; Indels 11; Gaps 10;

Db 49 yabphnslcctckhkytlvsdcpspgqetvcevdckgftlasqnhvrglscctcke 108  
 31 YDETSHQLLCDKCPGTYLKQHCCTAK-WKTVCAPCPDHYHTDSMHTSDCLCSPVCKE 89  
 109 mfyvelspckadmdtvcgckngfylysethgcvcddspcfng-tvllpckekqnlvcn 167  
 90 L-OYVQCECNRTNRYCECK-E-GRYL-EIEF-CLKHRSCTPGFGVQAGTEPRNTVCK 143

QY 168 -chagfflsgnecpschckngcc 191  
 144 RCPDGF-S-NETSKAPCKKHTNC 166

RESULT 12  
 ID NGRF.CHICK STANDARD; PRT; 416 AA.  
 AC P18519;  
 DT 01-NOV-1990 (REL. 16, CREATED)  
 DT 01-NOV-1990 (REL. 16, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)  
 DE (GP80-LNGFR).  
 OS GALLUS GALLUS (CHICKEN).  
 OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; AVES; NEOGNATHAE;  
 OC GALLIFORMES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-BRAIN;  
 RX MEDLINE: 90166579.  
 RA LARGE T.H., WESKAMP G., HELDER J.C., RADEKE M.J., MISKO T.P.,  
 RA SHOOTER E.M., REICHARDT L.F.;  
 RA NEURON 2:1123-1134(1989).  
 RL [2]  
 [2] SEQUENCE OF 21-416 FROM N.A.  
 MEDLINE: 90152140.  
 RA HEUER J.G., FATEME-NAINIE S., WHEELER E.F., BOTHWELL M.;  
 RA DEV. BIOL. 137:287-304(1990).  
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,  
 CC NT-3, AND NT-4.  
 CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE  
 CC BOND FORMATION.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR PIR: J00006; J00504.  
 DR PIR: A60504; A60504.  
 DR PROSITE: PS00652; TNFR\_NGFR.  
 DR RECEPTOR; PS00017; DEATH\_DOMAIN.  
 KW RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;  
 KW PHOSPHORYLATION; SIGNAL.  
 FT CHAIN 1 19 POTENTIAL.  
 FT CHAIN 20 416 NGF RECEPTOR.  
 FT DOMAIN 23 239 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 240 261 POTENTIAL.  
 FT DOMAIN 262 416 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 23 181 4 X TNFR-CYS.  
 FT REPEAT 23 57 TNFR-CYS 1.  
 FT REPEAT 58 100 TNFR-CYS 2.

FT REPEAT 101 140 TNFR-CYS 3.  
 FT REPEAT 141 181 TNFR-CYS 4.  
 FT DOMAIN 188 236 SER/THR-RICH.  
 FT DOMAIN 333 410 DEATH DOMAIN.  
 FT DISULFID 24 35 BY SIMILARITY.  
 FT DISULFID 36 49 BY SIMILARITY.  
 FT DISULFID 39 56 BY SIMILARITY.  
 FT DISULFID 59 75 BY SIMILARITY.  
 FT DISULFID 78 91 BY SIMILARITY.  
 FT DISULFID 81 99 BY SIMILARITY.  
 FT DISULFID 101 114 BY SIMILARITY.  
 FT DISULFID 117 130 BY SIMILARITY.  
 FT DISULFID 120 138 BY SIMILARITY.  
 FT DISULFID 141 156 BY SIMILARITY.  
 FT DISULFID 159 172 BY SIMILARITY.  
 FT DISULFID 162 180 BY SIMILARITY.  
 FT CARBOHYD 52 52 POTENTIAL.  
 FT CARBOHYD 36 36 C -> Y (IN REF. 2).  
 FT CONFLICT 173 173 T -> K (IN REF. 2).  
 FT CONFLICT 276 276 N -> S (IN REF. 2).  
 FT CONFLICT 396 396 K -> R (IN REF. 2).  
 SQ SEQUENCE 416 AA; 44654 MW; 4D3F086A CRC32;

Query Match 7.1%; Score 215; DB 6; Length 416;  
 Best Local Similarity 30.4%; Pred. No. 4.53e-22;  
 Matches 45; Conservative 27; Mismatches 70; Indels 6; Gaps 6;

Db 36 ckaenlgeyvvcpqyvn-qtvepcldsvlysdvatepckpctq-cvqjshmsapcve 93  
 41 CDKCPGTYLKQHCCTAKWKTVCAPCPDHY-YTDSMHTSDCLCSPVCKELOYKQECNR 99

Db 94 sddavrcaygyfdehlsqscscsicevgfqlmfrcdsqdtvceepgftsdantv 153  
 100 TNHRYCECKEGRYL-EIE-FCLHRSCTPGFGVQAGTEPRNTVCKRCPDGFSSNETSSK 157

QY 154 dplpcticeenwmyke-ctatsdaec 180  
 158 APCRKHNTCSVFGLLTKGNATHDNIC 185

RESULT 13  
 ID NGRF.HUMAN STANDARD; PRT; 427 AA.  
 AC P08138;  
 DT 01-AUG-1988 (REL. 08, CREATED)  
 DT 01-AUG-1988 (REL. 08, LAST SEQUENCE UPDATE)  
 DT 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)  
 DE (GP80-LNGFR).  
 OS NGFR.  
 OS HOMO SAPIENS (HUMAN).  
 OS EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 OC EUTHERIA; PRIMATES.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE: 87051725.  
 RA JOHNSON D., LANAHAN A., BUCK C.R., SERGAL A., MORGAN C., MERCER E.,  
 RA BOTHWELL M., CHAO M.;  
 RL CELL 47:545-554(1986).  
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,  
 CC NT-3, AND NT-4.  
 CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE  
 CC BOND FORMATION.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.  
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL: M14764; G189205; .  
 DR PIR: A25218; G0H0N.  
 DR HSSP: P19438; ITNR.  
 DR MIM: 162010; .  
 DR PROSITE: PS00652; TNFR\_NGFR.  
 DR PROSITE: PS00017; DEATH\_DOMAIN.  
 KW RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;  
 KW PHOSPHORYLATION; SIGNAL.

FT SIGNAL 1 28  
 FT CHAIN 29 427 NGF RECEPTOR.  
 FT DOMAIN 29 427 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 251 272 POTENTIAL.  
 FT DOMAIN 273 427 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 31 189 4 X TNFR-CYS.  
 FT REPEAT 31 65 TNFR-CYS 1.  
 FT REPEAT 66 107 TNFR-CYS 2.  
 FT REPEAT 108 147 TNFR-CYS 3.  
 FT REPEAT 148 189 TNFR-CYS 4.  
 FT DOMAIN 344 421 DEATH DOMAIN.  
 FT DISULFID 32 43 BY SIMILARITY.  
 FT DISULFID 44 57 BY SIMILARITY.  
 FT DISULFID 47 64 BY SIMILARITY.  
 FT DISULFID 67 83 BY SIMILARITY.  
 FT DISULFID 86 99 BY SIMILARITY.  
 FT DISULFID 109 122 BY SIMILARITY.  
 FT DISULFID 125 138 BY SIMILARITY.  
 FT DISULFID 128 146 BY SIMILARITY.  
 FT DISULFID 149 164 BY SIMILARITY.  
 FT DISULFID 167 180 BY SIMILARITY.  
 FT DISULFID 170 188 BY SIMILARITY.  
 FT DOMAIN 197 248 SER/THR-RICH.  
 FT CARBOHYD 60 POTENTIAL.  
 SQ SEQUENCE 427 AA; 45183 MW; EE2924BD CRC32;

Query Match 7.0%; Score 213; DB 6; Length 427;  
 Best Local Similarity 34.9%; Pred. No. 1,15e-21;

Matches 45; Conservative 19; Mismatches 60; Indels 5; Gaps 5;

Db 44 ckaenlgevgapcpgan-qtwcepldsvtsfadvstapckpcte-cvlglsmsapcve 101  
 Qy 41 CDKCPGTYLKHCHTAKMTVCAPCPDHY-YTDSMHTSDECLYCSPVCKELQYVQECNR 99  
 Db 102 addavcraygygdeetgrceacrvceagslvfscqdkntvcecpetgysdeanhv 161  
 Qy 100 THNRVCECKEGRYL-EI-EFLKHRSCPPGFGVQAGTPERNVCKRCPCDGFSSNETSSK 157  
 Db 162 dpcldpctvc 170  
 Qy 158 APCRKHTNC 166

RESULT 14  
 ID NGFR\_RAT STANDARD; PRT; 425 AA.  
 AC P071174;  
 DE 01-APR-1988 (REL. 07, CREATED)  
 RA 01-APR-1988 (REL. 07, LAST SEQUENCE UPDATE)  
 RA 01-NOV-1995 (REL. 32, LAST ANNOTATION UPDATE)  
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR) (GP80-LNGFR).  
 GN NGFR.  
 OS RATTUS NORVEGICUS (RAT).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; RODENTIA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 87115859.  
 RA RADEKE M.J., MISKO T.P., HSU C., HERZENBERG J.A., SHOOTER E.M.;  
 RA NATURE 325:593-597(1987).  
 RN [2]  
 RP SEQUENCE OF 1-22 FROM N.A.  
 RC TISSUE-LAYER;  
 RX MEDLINE; 93077038.  
 RA MEDSIS M., TIMMUSK T., ALLIKMETS R., SAARMA M., PERSSON H.;  
 RA GENE 121:247-254(1992).  
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,  
 CC NT-3, AND NT-4.  
 CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE  
 CC BOND FORMATION.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.

CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.  
 DR EMBL; X05137; G56756; -;  
 DR EMBL; X61269; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; A26431; A26431.  
 DR HSSP; P19438; TNFR.  
 DR PROSITE; PS00652; TNFR-NGFR.  
 DR PROSITE; PS50017; DEATH\_DOMAIN.  
 KW RECEPTOR; NEUROGENESIS; TRANSMEMBRANE; GLYCOPROTEIN; REPEAT;  
 KW PHOSPHORYLATION; SIGNAL.

FT SIGNAL 1 29  
 FT CHAIN 30 425  
 FT DOMAIN 30 251  
 FT TRANSMEM 252 273  
 FT DOMAIN 274 425  
 FT DOMAIN 32 190  
 FT REPEAT 32 66  
 FT REPEAT 67 108  
 FT REPEAT 109 148  
 FT REPEAT 149 190  
 FT DOMAIN 198 249  
 FT DOMAIN 354 419  
 FT DISULFID 33 44  
 FT DISULFID 45 58  
 FT DISULFID 48 65  
 FT DISULFID 68 84  
 FT DISULFID 87 100  
 FT DISULFID 90 108  
 FT DISULFID 110 123  
 FT DISULFID 126 139  
 FT DISULFID 129 147  
 FT DISULFID 150 165  
 FT DISULFID 168 181  
 FT DISULFID 171 189  
 FT CARBOHYD 61  
 FT CARBOHYD 71  
 SQ SEQUENCE 425 AA; 45432 MW; 7D7BF258 CRC32;

Query Match 6.8%; Score 207; DB 6; Length 425;  
 Best Local Similarity 33.3%; Pred. No. 1.87e-20;

Matches 43; Conservative 21; Mismatches 60; Indels 5; Gaps 4;

Db 45 ckaenlgevgapcpgan-qtwcepldsvtsfadvstapckpcte-cvlglsmsapcve 102  
 Qy 41 CDKCPGTYLKHCHTAKMTVCAPCPDHY-YTDSMHTSDECLYCSPVCKELQYVQECNR 99  
 Db 103 addavcraygygdeetgrceacrvceagslvfscqdkntvcecpetgysdeanhv 162  
 Qy 100 THNRVCECKEGRYL-EI-EFLKHRSCPPGFGVQAGTPERNVCKRCPCDGFSSNETSSK 157  
 Db 163 dpcldpctvc 171  
 Qy 158 APCRKHTNC 166

RESULT 15  
 ID FASA\_BOVIN STANDARD; PRT; 323 AA.  
 AC P51867;  
 DT 01-OCT-1996 (REL. 34, CREATED)  
 DT 01-OCT-1996 (REL. 34, LAST SEQUENCE UPDATE)  
 DT 01-OCT-1996 (REL. 34, LAST ANNOTATION UPDATE)  
 DE FAST RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS) (APO-1 ANTIGEN) (CD95).  
 GN APT1 OR FAS.  
 OS BOS TAURUS (BOVINE).  
 OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;  
 CC EUTHERIA; ARTIODACTYLA.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE; 96226401.  
 RA YOO J., STONE R.T., BEATTIE C.W.;  
 RA DNA CELL BIOL. 15:227-234(1996).  
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. MEDIATES  
 CC CELL DEATH. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE



CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED  
 CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).  
 CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC EMBL: U34794; G1262193; -.  
 DR APOPTOSIS; RECEPTOR; GLYCOPROTEIN; TRANSMEMBRANE; REPEAT; SIGNAL.  
 KW SIGNAL 1 16  
 FT CHAIN 17 323  
 FT DOMAIN 17 170  
 FT TRANSMEM 171 188  
 FT DOMAIN 189 323  
 FT DOMAIN 45 163  
 FT REPEAT 45 80  
 FT REPEAT 81 124  
 FT REPEAT 125 163  
 FT DOMAIN 222 302  
 SQ SEQUENCE 323 AA; 36445 MW; DA5A2A59 CRC32;

Query Match 6.2%; Score 188; DB 3; Length 323;

Best Local Similarity 35.7%; Pred. No. 1,08e-16; Mismatches 49; Indels 6; Gaps 6;

Db 53 hqfcccpgppgkirkngdckrdqdtpevcylcsegneytdkshndkciacs-icdeehgje 111  
 Oy 37 HQLLDKCPGPGTYLKHCHCAKMKTV-CAPCPD-HYTTDSMHTSDEGLYCSFVCKELQ-Y- 92  
 Db 112 veguctrtntkcrcksnfncnspspehnpcttcehgilekctptstnck 163  
 Oy 93 VKQECNRTHNRVCECKEGRYLEIFCLKHRSCP-GFGVVOAGTPERNTVCK 143

Search completed: Wed Aug 20 09:45:20 1997  
 Job time : 68 secs.

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